AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application:

List of Claims:

Claims 1- 27 (cancelled)

Claim 28 (Currently amended): A method of simultaneously genotyping multiple samples in a single round of hybridization, the method comprising:

1) incubating a microarray of polynucleotide samples from multiple individuals with a probe mixture of oligonucleotides of known sequence, wherein

a) the microarray contains a plurality of samples containing genotypes of interest with each sample in a distinct location and occupying an area smaller than about 1 square millimeter,

b) each sample has amplified polynucleotides with a defined segment containing a marker selected from a marker for a gene and markers for allelic variants of the gene,

c) the oligonucleotides in the probe mixture ~~consist of oligonucleotides~~ are of known sequence and length and ~~having~~ have sequences specifically complementary to polynucleotide sequences ~~those~~ within the defined segments for each sample for which a genotype is to be determined, wherein the oligonucleotides complementary to the polynucleotides are selected from the group consisting of oligonucleotides with sequences complementary to a segment containing the marker for (1) a gene, (2) one or more allelic variants of the gene, and (3) a gene and one or more allelic variants of the gene, and ~~also consisting essentially of, optionally, control oligonucleotides,~~

d) the incubating forms hybrids of polynucleotides of the microarray and complementary oligonucleotides and allows discrimination at single nucleotide resolution; and

2) detecting at the distinct location on the microarray after a single round of hybridization, stable hybrids formed during the incubation, wherein a hybridization signal indicating the formation of a hybrid or lack of formation of a hybrid ~~after a single round of hybridization at the distinct location is indicative of a genotype of~~ genotypes the individual.

Claim 29 (previously presented): The method of claim 28 wherein the polynucleotide samples of the microarray are amplification products.

Claim 30 (previously presented): The method of claim 29, wherein the amplification products are produced by a polymerase chain reaction (PCR) method.

Claim 31 (previously amended): The method of claim 30 wherein the plurality of samples of polynucleotides is at least 10.

Claim 32 (previously presented): The method of claim 28 wherein an allele of the gene is associated with a disease.

Claim 33 (previously presented): The method of claim 32 wherein the disease is a human disease.

Claim 34 (previously presented): The method of claim 32 wherein the gene is human and is selected from the group consisting of β-globin, Cystic Fibrosis Transmembrane Conductance Regulator (CFTR), and Galactose-1-Phosphate Uridyltransferase (Gal-1-PU).

Claim 35 (previously presented): The method of claim 28 wherein the microarray is on a surface containing at least 1000 locations per square centimeter.

Claim 36 (previously amended): The method of claim 28 wherein the probe mixture of oligonucleotides of known sequence comprises oligonucleotides with ten different sequences.

Claim 37 (previously presented): The method of claim 28 wherein the oligonucleotides in the mixture are between about 10 and 30 nucleotides in length.

Claim 38 (previously presented): The method of claim 28 wherein the distinct segment is between about 40 and about 1000 nucleotides.

Claim 39 (previously presented): The method of claim 28 wherein the incubating is in an aqueous solution comprised of salts and detergent.

Claim 40 (previously presented): The method of claim 28 wherein hybridizing is performed at a temperature about 10 °C below the melting temperature of the stable hybrids.

Claim 41 (previously presented): The method of claim 28 wherein the oligonucleotides of known sequence are labeled.

Claim 42 (previously presented): The method of claim 41 wherein the label is fluorescent.

Claim 43 (previously presented): The method of claim 28, wherein samples from homozygotes and samples from heterozygotes are distinguishable.

Claim 44 (previously amended): The method of claim 28 wherein the plurality of samples of polynucleotides is at least 5,000.

Claim 45 (previously presented): The method of claim 28 wherein the individual specimens are neonatal blood samples.

Claim 46 (previously amended): The method of claim 28 wherein the individual is a human.